

IN THE SPECIFICATION:

Kindly amend the specification as follows, in accordance with 37 C.F.R. § 1.121:

On page 2, please amend the paragraph starting at line 4 as follows:

Recently, expression profiles of strains in which genes coding global regulators such as the ArcA protein and Fnr protein derived from *E. coli* are disrupted are collected in a database by using DNA microarray techniques and opened to the public (~~http://www.genome.ad.jp/dbget-bin/get_htext?Exp_DB+n+Bget-bin/get_htext?Exp_DB+n+B~~) ([genome.ad.jp](http://www.genome.ad.jp)).

On page 6, please amend the paragraph starting at line 19, which continues to page 7, line 3, as follows:

The γ -proteobacterium used for the present invention is not particularly limited so long as it is a microorganism belonging to γ -proteobacteria such as genus *Escherichia*, *Enterobacter*, *Pantoea*, *Klebsiella*, *Serratia*, *Erwinia*, *Salmonella*, *Morganella* or the like and has an ability to produce a target substance. Specifically, those classified into the γ -proteobacteria according to the taxonomy used in the NCBI (National Center for Biotechnology Information) database (~~<http://www.ncbi.nlm.nih.gov/htbin-post/Taxonomy/wgetorg?mode=Tree&id=1236&lvl=3&keep=1&srchmode=1&unloc>~~ ~~[k ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)~~) can be used.

On page 25, please amend the paragraph starting at line 9 as follows:

The entire nucleotide sequence of genomic DNA of *E. coli* K-12 strain has been already elucidated (Blattner F.R., Plunkett G., Bloch C.A. et al., Science, 227, 1453-1474 (1997); ~~<ftp://ftp.genetics.wisc.edu/pub/sequence/ecolim52.seq.gz>~~ genetics.wisc.edu). Based on the known nucleotide sequences of *arcA*, *dam* and *fnr* genes, gene-disrupted strains for each of *arcA*, *dam* and *fnr* were produced. In the following procedure, QUAGEN-Genomic-tip System (produced by QIAGEN) was used for the extraction of genomic DNA.